

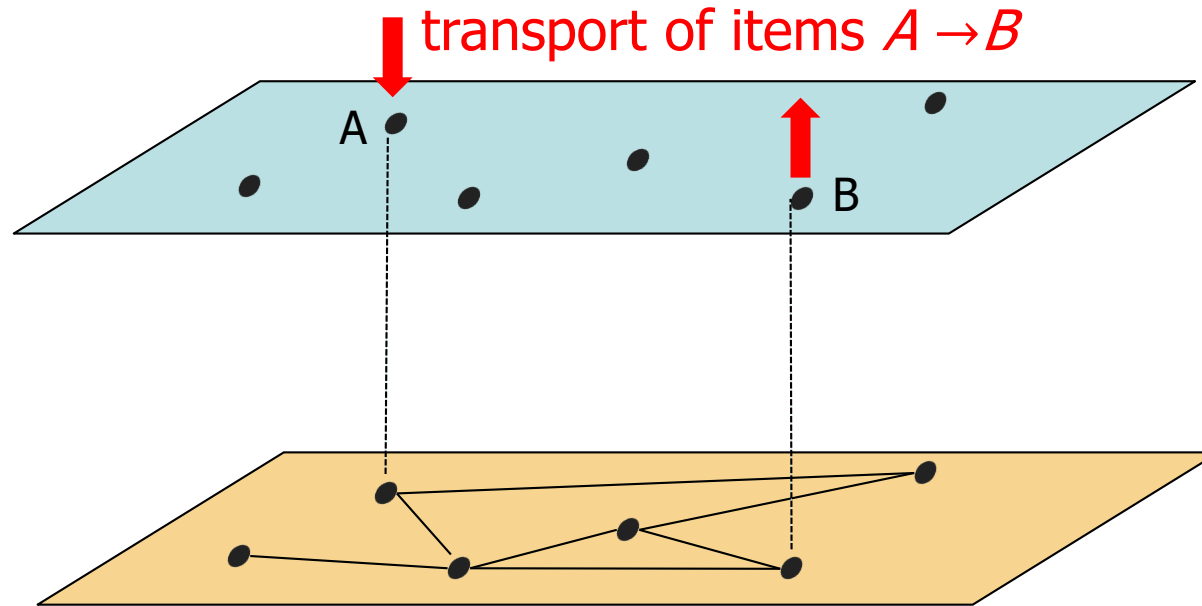
Prediction of the Epidemic Nodal State from Reported data

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in collaboration with

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Network = Process + Graph



Process (Function)

Software, service

Graph (Structure)

Hardware, Topologie
Relationship between items
and/or processes

Network Science: Theory of processes on/in graphs



Duality between process and graph is a cornerstone

Epidemics on Networks in brief

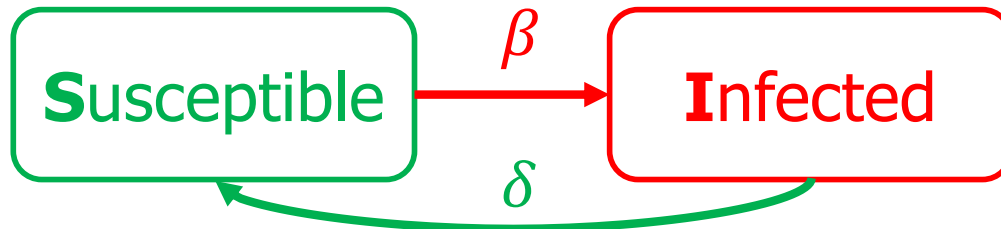
- Closed population with N individuals:
 - Accurate models for any compartment on any *fixed* graph (mean-field approximation & Markovian setting)
 - *Open*:
 - non-Markovian
 - time-varying networks
 - adaptive networks
- Open population:
 - In contrast to classical epidemics, hardly any network science paper
 - Complication: graph with variable number of nodes

Epidemic “compartments”

Single disease realization



Diseases with re-infections



Essence: item can only be in 1 compartment at time t

SIS Mean-field Equations in discrete time k

Difference equation of infection probability $I_i[k]$ of node i :

$$I_i[k + 1] = \underbrace{(1 - \delta_i)I_i[k]}_{\text{curing}} + \underbrace{(1 - I_i[k]) \sum_{j=1}^N \beta_{ij} I_j[k]}_{\text{infections}}$$

δ_i : Curing probability of group i ($N \times 1$ vector δ)

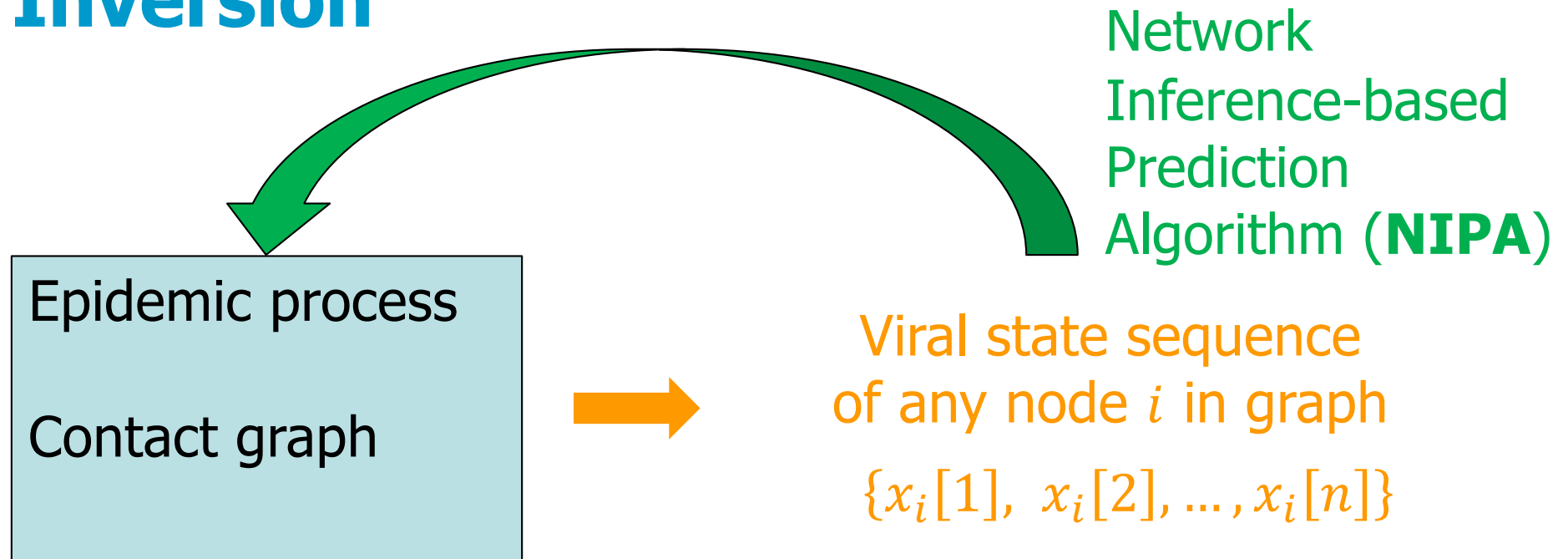
β_{ij} : Infection probability from group j to group i ($N \times N$ matrix B)

Non-linear in vector $I[k]$, but **linear** in vector δ and matrix B

Prasse, B. and P. Van Mieghem, 2019, "The Viral State Dynamics of the Discrete-Time NIMFA Epidemic Model", IEEE Transactions on Network Science and Engineering, to appear.

Prasse, B. and P. Van Mieghem, 2020, "Network Reconstruction and Prediction of Epidemic Outbreaks for General Group-Based Compartmental Epidemic Models", IEEE Transactions on Network Science and Engineering, to appear.

Inversion

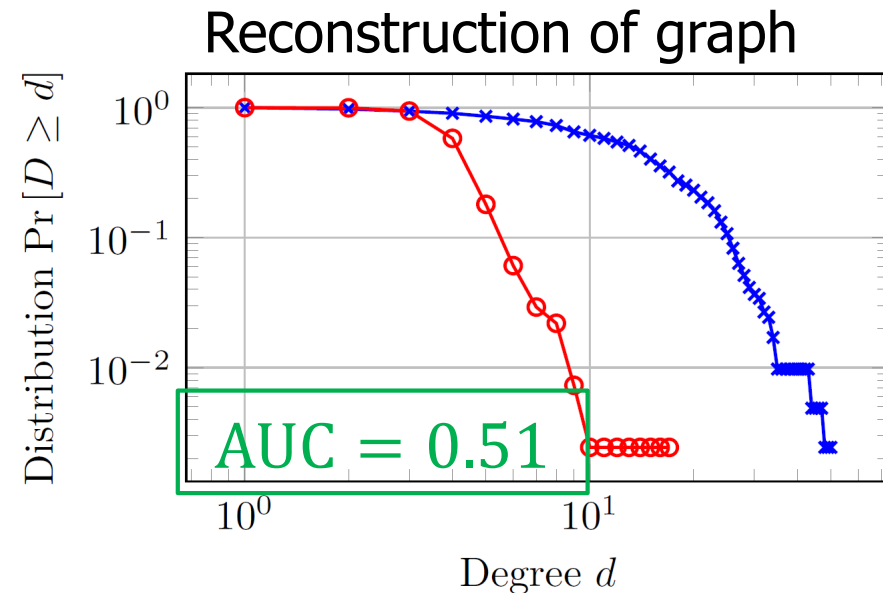
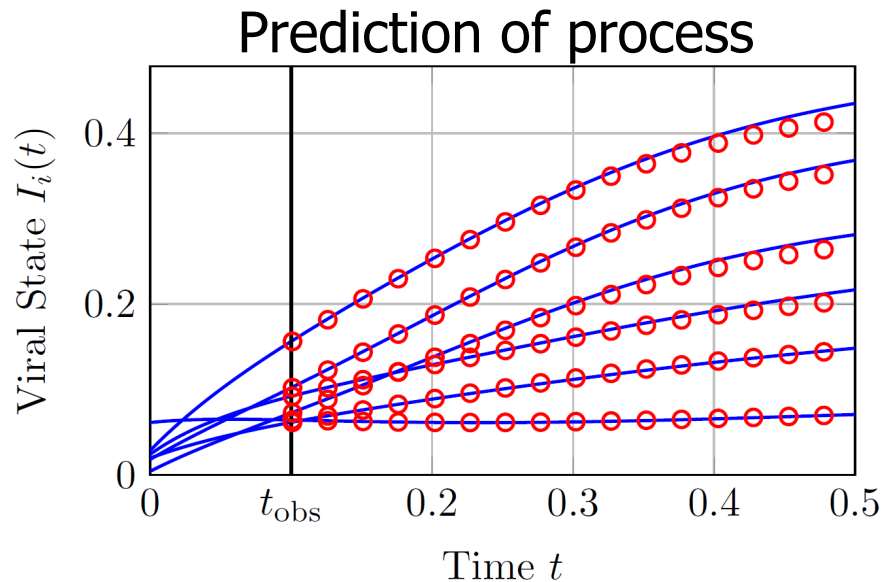


Linear, but **seriously underdetermined** problem

Optimization with constraints (Lagrange's multipliers):

- very effective numerical techniques
- beyond Gauss's least square criterion (e.g. LASSO)

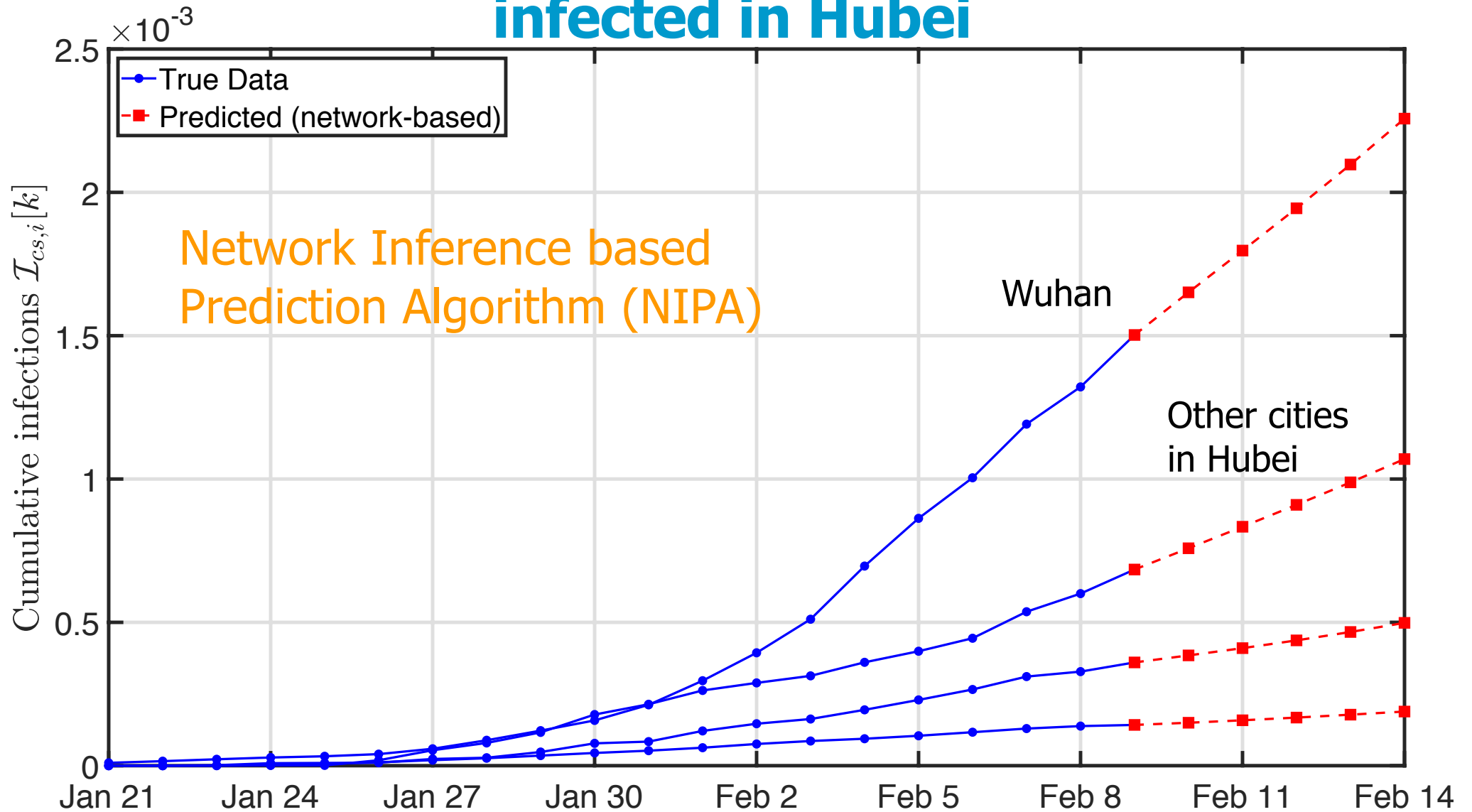
Excellent prediction *process*; bad *graph*



Accurate prediction of network dynamics ***without*** knowing the network's topology

Reason: one virus outbreak agitates few network dynamical modes. Not only for epidemics but also e.g. : Population dynamics (Lotka-Volterra), Gene regulatory dynamics (Michaelis-Menten), Neural firing (Wilson-Cowan)

Expected Cumulative Fraction of COVID-19 infected in Hubei



Conclusion

- Given infected data in space (network) & time:
 - Accurate **short-time** predictions **possible with NIPA**
 - Accurate **long-time** predictions **hardly possible**

Discussion panel (observations):

- Insufficient measurements (“meten = weten”)
- Digital technology (e.g. apps on smart phone, base-stations, sensors, etc.)
 - Insufficiently exploited (privacy)
 - Less costly than vaccine development
- No optimized “COVID-19” strategy
 - Each country claims the best method
- Political choices in triangle *freedom-health-economy*



Thank You

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